

HIV and Cellular Factors

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Introduction

Viruses are obligatory parasites of cells. Thus it is expected that host cell factors contribute importantly to the life-cycle of viruses. In this section, we survey, for HIV-1, four types of virus-cell interactions. These four areas include: 1) DNA-binding proteins that recognize target motifs in proviral LTR; 2) RNA-binding proteins that bind HIV-1 RNAs; 3) cellular factors that form protein-protein complexes with HIV-1 regulatory proteins; and 4) cellular genes which are modulated upon viral infection. With rapid increases in knowledge in the area of virus-cell interactions, we anticipate that this initial survey would be expanded extensively in future editions of the data base. Additional discussions on HIV-cell interactions are found elsewhere (Jones and Peterlin, 1994; Jeang and Gatignol, 1994; Garcia and Gaynor, 1994; Gatignol *et al.*, 1996; Dayton, 1996).

I. DNA-binding Proteins

The promoter-enhancers of the human immunodeficiency virus (HIV) are contained in the U3 of the viral long terminal repeat (LTR). HIV-1 U3 is typically 454 nucleotides long and has binding sites for many transcription factors. Some of these are diagrammed in figure 1. With the exception of NF- κ B and Sp1 (Ross *et al.*, 1991; Kim *et al.*, 1993; Huang and Jeang, 1993; Huang *et al.*, 1994), verification of the importance of the various sequences in viral contexts has not been directly performed.

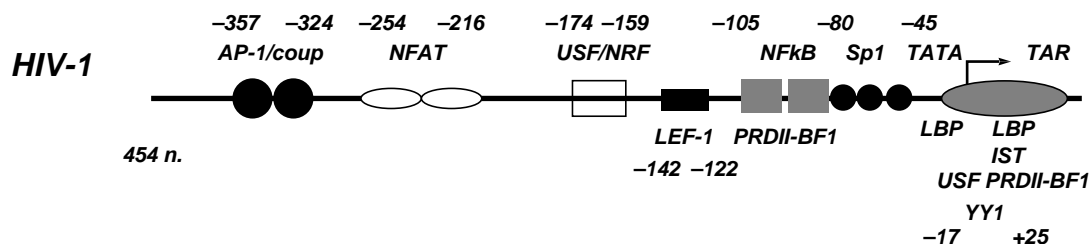


Fig. 1. Diagrammatic representation of the positions in U3 and R for some of the DNA-binding proteins that recognize the HIV-1 LTR.

Subgenomic assays in cultured cells indicate that the primary contributors to HIV-promoter activity are the NF- κ B, Sp1, and TATAA (sequences from +1 to -105; Berkhout and Jeang, 1992). Nonetheless, it is likely that other DNA-binding factors also contribute *in vivo*. Beginning directionally from the 5' end of U3, binding sites for AP-1 (a fos/jun hetero-complex; van Straaten *et al.*, 1983; Hattori *et al.*, 1988) and COUP (a member of the steroid/thyroid receptor superfamily; Cooney *et al.*, 1991) are found between -324 to -357. Both COUP and AP-1 are expressed in human T-cells, and thus could compete with each other for the same proviral DNA sites during HIV-1 infection.

More proximally, between -216 and -254 are binding motifs for nuclear factor from activated T-cells (NFAT; Shaw *et al.*, 1988). NFAT is an intermediating transducer of signals initiated at the T-cell antigen receptor. Recent evidence suggests that NFAT binding activity is composed of three discrete polypeptides, NFATp (McCaffrey *et al.*, 1993), Fos and Jun (Yaseen *et al.*, 1993).

In the region between –159 to –174 is a binding consensus sequence for USF (Gregor *et al.*, 1990). USF was characterized initially as a positive activator of adenovirus major-late-promoter transcription. In the HIV context, there is conflicting information on whether this factor has moderating (and thus be regarded as a negative regulatory factor; NRF; Lu *et al.*, 1990) or stimulating (Maekewa *et al.*, 1991) effects. Interestingly, USF also binds a second unrelated sequence (–5 to +11) that surrounds the HIV-1 initiator (Hu *et al.*, 1993). USF interaction at the initiator-proximal site activates strong expression from the TATAA-promoter (Hu *et al.*, 1993). Of note, a factor distinct from USF, but which binds the same DNA-sequence, has also been cloned and characterized (TFE3; Bechmann and Kadesch, 1991).

LEF-1 is a T-cell specific transcription factor (Waterman and Jones, 1990). Once bound to its cognate site, LEF-1 bends DNA and thereby facilitates the assembly of nucleoprotein complexes at the promoter (Giese *et al.*, 1992; reviewed in Jones and Peterlin, 1994). A high affinity LEF-1 binding site is present at –122 to –143. Two low affinity binding sites exist at –37 to –51 and +17 to +32 (Waterman and Jones, 1990).

NF- κ B (Nabel and Baltimore, 1987) and Sp1 (Jones and Tjian, 1985; Jones *et al.*, 1986) motifs are perhaps the best characterized sequence elements in the HIV-1 LTR. These sequences directly impact viral replication (Ross *et al.*, 1991; Kim *et al.*, 1993; Huang and Jeang, 1993; Huang *et al.*, 1994), viral transcription (Harrich *et al.*, 1990; Berkhout and Jeang, 1992; Pazin *et al.*, 1996), and Tat transactivation (reviewed in Jones and Peterlin, 1994; Jeang and Gagnon, 1994). For more extensive discussions of the biochemical and functional properties of NF- κ B (Ghosh *et al.*, 1990; Kieran *et al.*, 1990; Nolan *et al.*, 1991; Liou *et al.*, 1991; and references cited therein) and Sp1 (Dyran and Tjian, 1983; Briggs *et al.*, 1986; Kadonaga *et al.*, 1987; and references cited therein), readers should consult elsewhere.

PRDII-BF1 is a 300 kDa zinc-finger containing protein (Baldwin *et al.*, 1990; Seeler *et al.*, 1994). PRDII-BF1 recognizes and binds the NF- κ B motif; however, it also binds a divergent sequence in R (+27 to +52; Seeler *et al.*, 1994).

Positioned at the junction of U3 and R are sites for LBP (Yoon *et al.*, 1994) and YY1 (Useheva and Shenk, 1994; Seto *et al.*, 1991). While the role for LBP in HIV-1 transcription is not wholly understood (Jones *et al.*, 1988; Kato *et al.*, 1991), binding of YY1 to the LTR has been shown to repress HIV-1 expression and production of virions (Margolis *et al.*, 1994). Besides LBP and YY1, a DNA-mediated activity for the induction of short transcripts (IST) has also been mapped to the same general vicinity (–5 to +26; Sheldon *et al.*, 1993). The cDNA for the cellular factor that mediates IST-activity has not been isolated, and thus the authentic identity of this factor is unknown. HIP 116 is another newly cloned cDNA that binds to the TATA/initiator of the HIV-1 promoter (Sheridan *et al.*, 1995).

There are a number of reports of sites for DNA-binding proteins in the HIV-1 genome that occur downstream of the +1 start for transcription. These include NF- κ B motifs (Mallardo *et al.*, 1996) and sites for AP-1, AP-3-like, DBF-1, and Sp-1 (El Kharroubi and Martin, 1996). The full implication of these downstream DNA-motifs in the setting of HIV-1 infection remains to be clarified.

II. RNA-binding Proteins

In recent years, it has become evident that RNA-binding proteins play important roles in gene regulation (see reviews, Keene and Query, 1991; Mattaj, 1993; Burd and Dreyfuss, 1994). For HIV-1, cellular proteins that bind viral regulatory RNAs have been studied in detail. In particular, at least eight host cell factors have been described to bind TAR RNA. Similarly, two RRE-binding factors have been characterized. There are also biologically compelling reasons as to why TAR- and RRE- binding proteins are meaningful contributors to the HIV-1 lifecycle.

The HIV-1 leader RNA, TAR, forms a stem-bulge-loop structure of approximately 60+ nucleotides (Muesing *et al.*, 1987; Berkhout and Jeang, 1989). Early, it was reported that many human cellular proteins bound TAR RNA (Gagnon *et al.*, 1989; Gaynor *et al.*, 1989). Since then, some of these factors have been defined further. Tabulating from extant studies, eight proteins associate with either the bulge, loop, or stem of TAR RNA (see fig. 2). TAR loop-binding proteins include p68 (Marciniak *et al.*, 1990), and TRP1/TRP185 (185 kDa; Sheline *et al.*, 1991; Wu *et al.*, 1991), while TRP2 (70–110 kDa; Sheline *et al.*, 1991) binds to TAR-bulge. Proteins that complex with the double-stranded stem of TAR RNA

consist of P1/dSI (newly renamed as PKR; McCormack *et al.*, 1992; Roy *et al.*, 1991), SBP (140 kDa; Rounseville and Kumar, 1992), and TRBP (Gatignol *et al.*, 1991; Gatignol *et al.*, 1993). Two human autoantigens have been identified as TAR RNA-binding factors: Lupus antigen Ku (Kaczmarek and Khan, 1993) binds to the loop of TAR, while La (Chang *et al.*, 1994; Svitkin *et al.*, 1994) recognizes U-residues within the overall context of the TAR secondary structure.

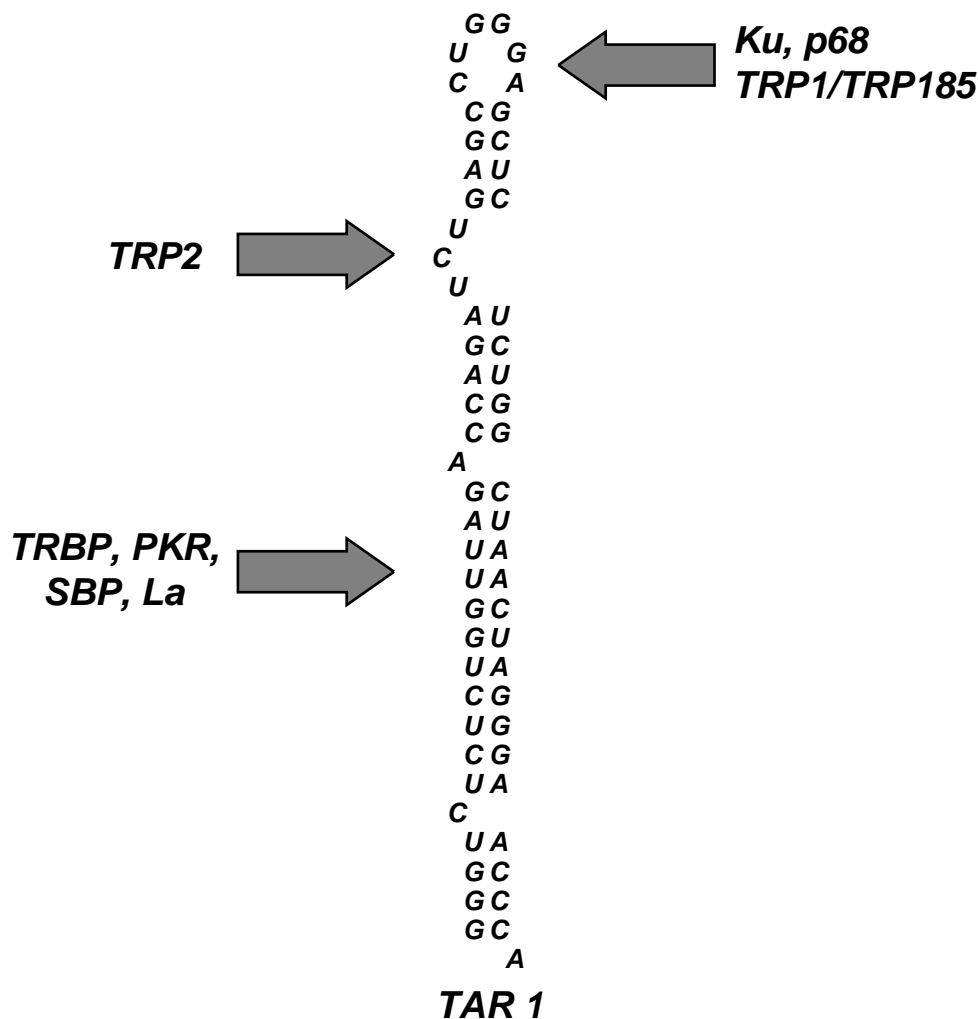


Fig. 2. Structure of the HIV-1 TAR RNA. Identities of the proteins that bind to the loop, bulge or stem of the TAR hairpin are indicated.

Recently, additional TAR-RNA-binding proteins and co-factors have been reported. Wong-Staal and colleagues have described the binding of TARBP-b (Reddy *et al.*, 1995) to the bulge structure of TAR. A set of cellular co-factors that enhances the binding of TRP 185 and RNA polymerase II (RNAP II) to TAR have been described by Gaynor and colleagues (Wu-Baer *et al.*, 1996a; 1996b). Finally, Hart and co-workers have characterized the elusive human chromosome 12-associated TAR loop-binding factor as an 83-kilodalton primate cell-specific protein whose expression is constitutively absent in hamster cells (Hart *et al.*, 1995).

RRE-binding proteins have also been studied extensively. We know that TRBP also can bind RRE (Park *et al.*, 1994). A 56 kDa factor (Vaishnav *et al.*, 1992) and a 49 kDa protein that belongs to

the heterogeneous nuclear ribonuclear protein family (Xu *et al.*, 1996) have been reported to bind RRE. Two other factors of 120 kDa and 60 kDa in molecular size have been reported to be primate-specific RRE-binding factors that are not expressed in rodent cells (Shukla *et al.*, 1994). It is expected that other RRE-factors would emerge from future studies. How these, as yet poorly characterized, factors might contribute to Rev/RRE function is reviewed in detail elsewhere (Dayton, 1996).

III. Protein-protein interactions

Protein-protein interactions are well-documented to be important in gene regulation (see reviews, Lewin, 1990; Greenblatt, 1991). Recent studies suggest that many HIV-1 proteins complex with host cell factors. We briefly describe below some examples pertaining to Tat, Rev, Gag, and Nef.

Although Tat is best known for transcription, it has other functions (Huang *et al.*, 1994; reviewed in Chang *et al.*, 1995; Goldstein, 1996) and has been reported to be a secretable factor that promotes the growth of Kaposi-like cells (Ensoli *et al.*, 1990). There is evidence that Tat can be taken up actively into cells (Frankel and Pabo, 1988) through binding to a cell-surface protein (Weeks *et al.*, 1993) implicated to be $\alpha_v\beta_5$ integrin (Vogel *et al.*, 1993). Once inside cells, Tat interacts with multiple partners in activating transcription (see also Tat Structure and Function section; Part III).

Two factors that bind Tat are themselves critical components of the eucaryotic RNA polymerase II transcription machinery. Genetic evidence supports a critical role for Sp1 in HIV-1 Tat-mediated transactivation (Harrich *et al.*, 1989; Kamine *et al.*, 1991; Southgate and Green, 1991; Berkhout and Jeang, 1992). Interestingly, direct protein-protein interactions between Tat and Sp1 (Jeang *et al.*, 1993) and Tat and the thyroid hormone receptor (which in certain cells bind at the Sp1 sites in the HIV-1 LTR; Desai-Yajnik *et al.*, 1995) have been documented. In addition, there is evidence that Tat also contacts TBP (Kashanchi *et al.*, 1994) and that Tat-Sp1-TFIID could present as a multiprotein complex (Huang *et al.*, 1993) inside cells. The critical nature of Tat-TBP contact has been questioned recently (Wang *et al.*, 1996). These investigators found that a trans-activation defective Tat protein bound TBP with the same avidity as wild type Tat protein, suggesting that binding to TBP cannot solely reflect the trans-activation property of Tat.

A large family of proteins related to the 26S protease from human erythrocytes (Dubiel *et al.*, 1994) are Tat-binding polypeptides. Members of this family include TBP-1 (Nelbock *et al.*, 1990; Ohana *et al.*, 1993), TBP-7 (Ohana *et al.*, 1993; Shaw and Ennis, 1993), MSS1 (Shibuya *et al.*, 1992), and SUG1 (Swaffield *et al.*, 1992). The exact role of this family of proteins in cellular metabolism is not wholly clear; however, the 26S protease seems to regulate the degradation of some cyclins and in this manner has been implicated in modulating the stability of oncoproteins such as c-Mos, c-Myb, c-Myc and p53 (Dubiel *et al.*, 1994).

Other cellular proteins, a 36 kDa protein (Desai *et al.*, 1991), a 60 kDa protein (Kamine *et al.*, 1996), and different cellular protein kinases (Hermann and Rice, 1993; McMillan *et al.*, 1995; Zhou and Sharp, 1996; Chun and Jeang, 1996), have been reported to bind Tat. Mavankal and colleagues have suggested that RNA polymerase II (RNAP II) is itself a specific Tat-binding protein (Mavankal *et al.*, 1996). The findings that RNAP II and kinases that phosphorylate RNAP II are Tat-binding factors suggest that these components contribute a part to explaining Tat function in transcription.

Multiple cellular factors also interact with Rev. Rev localizes to the nucleoli, and work by Laemmli and colleagues (Fankhauser *et al.*, 1991) and others (Miyazaki *et al.*, 1995; Szebeni *et al.*, 1995) have demonstrated a tight association between the basic nuclear-localizing domain of Rev and nucleolar B23 protein. This protein-protein complex likely directs the subcellular localization of Rev.

By contrast, many investigators have studied the nuclear export function of Rev (Fischer *et al.*, 1994; 1995; Wen *et al.*, 1995; Myer *et al.*, 1996; Fridell *et al.*, 1996). Using the yeast two-hybrid cloning approach, three groups have isolated closely related nucleoporin proteins that bind wild type but not mutant Rev (Fritz *et al.*, 1995; Bogerd *et al.*, 1995; Stutz *et al.*, 1995). These results suggest that the nucleoporin class of proteins are the Rev activation-domain specific co-factors involved in the nuclear to cytoplasmic export of RNAs.

Rev function can also be modulated by associations with other cellular factors. Two additional proteins have been shown to bind Rev. These are translation factor eIF-5A (Ruhl *et al.*, 1993; Bevec *et al.*, 1996), and serine-arginine (SR)-rich factors (Gontarek and Derse, 1996) such as the p32 protein (Luo *et al.*, 1994; Tange *et al.*, 1996) originally characterized by Krainer and colleagues (Krainer *et al.*, 1991) as a splicing factor-SF2-associated polypeptide. SR-rich proteins can also bind to the basic domain of the HIV-1 and HIV-2 Tat proteins (Trinh and Jeang, unpublished observation; B.R. Cullen, personal communication).

Other less-characterized Rev-binding proteins include human prothymosin alpha (Kubota *et al.*, 1995) and nuclear lamin B (Nikolakaki *et al.*, 1996).

Both HIV Gag and Nef also have cellular partners. p55 and p24 Gag bind cyclophilin A and cyclophilin B proteins (Luban *et al.*, 1993). The cyclophilins are cellular polypeptides originally characterized for their specific binding to cyclosporin A.

Nef has been found to bind β -COP, a coat protein from non-clathrin-coated vesicles (Benichou *et al.*, 1994). This interaction may be important in promoting the intracellular sequestration of CD4. Nef has also been shown to interact directly with CD4 (Rossi *et al.*, 1996). Recently many kinases have been described to associate with Nef (Sawai *et al.*, 1994; Saksela *et al.*, 1995; Bodeus *et al.*, 1995; Luo and Garcia, 1996). The identity of some of these kinases include Lck (Salghetti *et al.*, 1995; Collette *et al.*, 1996), Hck (Lee *et al.*, 1995), and PAK (Nunn and Marsh, 1996). Undoubtedly, there is much more to be learned from this area of research.

IV. Cellular Genes Modulated by HIV

Infection of cells by HIV results in activation and repression of many cellular genes. Because of the complexity of ambient gene expression inside cells, it is logistically difficult to dissect those genes that are upregulated from those that are downregulated from others that remain unperturbed. Nevertheless, several examples of genes that respond to HIV infection are known. Some of these include IL-2 (Westendorf *et al.*, 1994), IL6 (Scala *et al.*, 1994), and TGF- β (Buonaguro *et al.*, 1994; Rasty *et al.*, 1996).

Recent investigations have shown that HIV-1 proteins such as Tat and Nef potentially affect cellular metabolism. Tat, for example, has been shown to modulate the expression of cytokines including MIP-1 alpha (Sharma *et al.*, 1996), second messengers including nitric oxide (Barton *et al.*, 1996), and housekeeping genes such as Bcl2 (Zauli *et al.*, 1995a). Both Tat and Nef participate in signal transduction pathways that include NF- κ B (Demarchi *et al.*, 1996), phosphatidylinositol kinase (Zauli *et al.*, 1995b; Gramagli *et al.*, 1996), and protein kinase C (Conant *et al.*, 1996).

The identification of genes modulated by HIV has been based on classical approaches; however, with the advent of mRNA differential display technology (Liang and Pardee, 1992) the exhaustive characterization of cellular genes that respond to infection by HIV should be accomplished with greater ease. One such example has recently been reported. Zeichner and colleagues, using a differential display approach, found that expression of the human glucose transporter protein (GLUT3) is upregulated by HIV-1 infection. We anticipate reports on others, shortly.

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